(3) At column 32, delete Table IV and replace it with:

TABLE IV

Seven Different Versions of the 20-Amino Acid Repeat

Consensus:	F*VE*TP*CFSR*SSLSSLS	(SEQ ID NO:147)
1262:	YCVEDTPICFSRCSSLSSLS	(SEQ ID NO:148)
1376:	HTVQETPLMFSRCTSVSSLD	(SEQ ID NO:149)
1492:	FATESTPDGFSCSSSLSALS	(SEQ ID NO:150)
1643:	YCVEGTPIMFSTATSLSDLT	(SEQ ID NO:151)
1848:	TPIEGTPYCFSRNDSLSSLD	(SEQ ID NO:152)
1953:	FAIENTPVCPSHNSSLSSLS	(SEQ ID NO:153)
2013:	RHVEDTPVCFSRNSSLSSLS	(SEQ ID NO:154)

Numbers denote the first amino acid of each repeat. The consensus sequence at the top reflects a majority amino acid at a given position.

(4) Delete the sequence listing originally filed with the application and replace it with the paper copy of the substitute sequence listing that accompanies this amendment.

Remarks

The Second Advisory Action mailed December 28, 2001 indicated that the sequences of Tables III and IV must be identified by SEQ ID NO: before the application can be allowed. This amendment provides sequence identifiers for each of the sequences in Tables III and IV.

The amendment also provides a substitute seqence listing. The substitute sequence listing adds sequences in Tables III and IV that were not present in the sequence listing filed with the application. In addition, the sequence listing makes two clerical corrections to SEQ ID NOS:68 and 76 ("C" instead of "G" at position 24 of SEQ ID NO:68 and "C" instead of "G" at position 20 of SEQ ID NO:76). These sequences were corrected to conform to the sequences

designated as SEQ ID NO:68 and SEQ ID NO:76 in Table III.

Neither the amendments to the specification nor the substitute sequence listing adds new matter.

A paper copy and a computer readable form of the sequence listing accompany this amendment. I believe the contents of the paper and computer readable forms are identical.

Respectfully submitted,

Date: March 8, 2002

By: Lisa M. Hemmendinger
Lisa M. Hemmendinger
Registration No. 42,653

Banner & Witcoff, Ltd.
1001 G Street, N.W., Eleventh Floor
Washington, D.C. 20001-4597
(202) 508-9100

Appendix 1. Version of the amended paragraphs, with markings to show changes made.

(1) Column 26, lines 28-42:

C1

To obtain DNA sequence adjacent to the exons of the genes DP1, DP2.5, and SRP19, sequencing substrate was obtained by inverse PCR amplification of DNAs from two YACs, 310D8 and 183H12, that span the deletions. Ligation at low concentration cyclized the restriction enzyme-digested YAC DNAs. Oligonucleotides with sequencing tails, designed in inverse orientation at intervals along the cDNAs, primed PCR amplification from the cyclized templates. Comparison of these DNA sequences with the cDNA sequences placed exon boundaries at the divergence points. SRP19 and DP1 were each shown to have five exons. DP2.5 consisted of 15 exons. The sequences of the oligonucleotides synthesized to provide PCR amplification primers for the exons of each of these genes are listed in Table III [SEQ ID NO:39-94].

(2) Columns 26-27 (all underlining *except* that under the sequence identifiers was present in the original Table III):

Table III

Sequence of Primers Used for SSCP Analyses

Exon	Primer 1	Primer 2
	DP1	
	UP-TCCCCGCCTGCCGCTCTC (SEQ ID NO:39)	RP-GCAGCGGCGGCTCCCGTG (SEQ ID NO:40)
	UP-GTGAACGGCTCTCATGCTGC (SEQ ID NO:41)	RP-ACGTGCGGGGAGGAATGGA (SEQ ID NO:42)
	UP-ATGATATCTTACCAAATGATATAC (SEQ ID NO:43)	RP-TTATTCCTACTTCTTCTATACAG (SEQ ID NO:44)
	UP-TACCCATGCTGGCTCTTTTTC (SEQ ID NO:45)	RP-TGGGGCCATCTTGTTCCTGA (SEQ ID NO:46)
	UP-ACATTAGGCACAAAGCTTGCAA (SEQ ID NO:47)	RP-ATCAAGCTCCAGTAAGAAGGTA (SEQ ID NO:48)
	SRP19	
	UP-TGCGGCTCCTGGGTTGTTG (SEQ ID NO:49)	RP-GCCCCTTCCTTTCTGAGGAC (SEQ ID NO:50)
	UP-TTTTCTCCTGCCTCTTACTGC (SEQ ID NO:51)	RP-ATGACACCCCCCATTCCCTC (SEQ ID NO:52)
	UP-CCACTTAAAGCACATATATTTAGT (SEQ ID NO:53)	RP-GTATGGAAAATAGTGAAGAACC (SEQ ID NO:54)
	UP-TTCTTAAGTCCTGTTTTTCTTTTG (SEQ ID NO:55)	RP-TTTAGAACCTTTTTTGTGTTGTG (SEQ ID NO:56)
	UP-CTCAGATTATACACTAAGCCTAAC (SEQ ID NO:57)	RP-CATGTCTCTTACAGTAGTACCA (SEQ ID NO:58)
	DP2.5	
	UP-AGGTCCAAGGGTAGCCAAGG* (SEQ ID NO:59)	RP-TAAAAATGGATAAACTACAATTAAAAG (SEQ ID NO:60)
	UP-AAATACAGAATCATGTCTTGAAGT (SEQ ID NO:61)	RP-ACACCTAAAGATGACAATTTGAG (SEQ ID NO:62)
	UP-TAACTTAGATAGCAGTAATTTCCC* (SEQ ID NO:63)	RP-ACAATAAACTGGAGTACACAAGG (SEQ ID NO:64)
	UP-ATAGGTCATTGCTTCTTGCTGAT* (SEQ ID NO:65)	RP-TGAATTTTAATGGATTACCTAGGT (SEQ ID NO:66)
	UP-CTTTTTTTGCTTTTACTGATTAACG (SEQ ID NO:67)	RP-TGTAATTCATTTTATTCCTAATACCTC (SEQ ID NO:68)
	UP-GGTAGCCATAGTATGATTATTTCT (SEQ ID NO:69)	RP-CTACCTATTTTTATACCCACAAAC (SEQ ID NO:70)
	UP-AAGAAAGCCTACACCATTTTTGC (SEQ ID NO:71)	RP-GATCATTCTTAGAACCATCTTGC (SEQ ID NO:72)
	UP-ACCTATAGTCTAAATTATACCATC (SEQ ID NO:73)	RP-GTCATGGCATTACTGACCAG (SEQ ID NO:74)
	UP-AGTCGTAATTTTGTTTCTAAACTC (SEQ ID NO:75)	RP-TGAAGGACTCCGATTTCACCC* (SEQ ID NO:76)

Cont. C2

	UP-TCATTCACTCACAGCCTGATGAC* (SEQ ID NO:77)	RP-GCTTTGAAACATGCACTACGAT (SEQ ID NO:78)
	UP-AAACATCATTGCTCTTCAAATAAC (SEQ ID NO:79)	RP-TACCATGATTTAAAAATCCACCAG (SEQ ID NO:80)
	UP-GATGATTGTCTTTTTCCTCTTTGC (SEQ ID NO:81)	RP-CTGAGCTATCTTAAGAAATACATG (SEQ ID NO:82)
	UP-TTTTAAATGATCCTCTATTCTGTAT (SEQ ID NO:83)	RP-ACAGAGTCAGACCCTCCCTCAAAG (SEQ ID NO:84)
	UP-TTTCTATTCTTACTGCTAGCATT (SEQ ID NO:85)	RP-ATACACAGGTAAGAAATTAGGA (SEQ ID NO:86)
	UP-TAGATGACCCATATTCTCTTTC (SEQ ID NO:87)	RP-CAATTAGGTCTTTTTGAGAGTA (SEQ ID NO:88)
3-A	UP-GTTACTGCATACACATTGTGAC (SEQ ID NO:89)	RP-GCTTTTTGTTTCGTAACATGAAG* (SEQ ID NO:90)
B	UP-AGTACAAGGATGCCAATATTATG* (SEQ ID NO:103)	RP-ACTTCTATCTTTTTCAGAACGAG* (SEQ ID NO:104)
C	UP-ATTTGAATACTACAGTGTTACCC* (SEQ ID NO:105)	RP-CTTGTATTCTAATTTGGCATAAGG* (SEQ ID NO:106)
D	UP-CTGCCCATACACATTCAAACAC* (SEQ ID NO:107)	RP-TGTTTGCGTCTTGCCCATCTT* (SEQ ID NO:108)
E	UP-AGTCTTAAATATTCAGATGAGCAG* (SEQ ID NO:109)	RP-GTTTCTCTTCATTATATTTTATGCTA* (SEQ ID NO:110)
F	UP-AAGCCTACCAATTATAGTGAACG* (SEQ ID NO:111)	RP-AGCTGATGACAAAGATGATAATC* (SEQ ID NO:112)
G	UP-AAGAAACAATACAGACTTATTGTG* (SEQ ID NO:113)	RP-ATGAGTGGGGTCTCCTGAAC* (SEQ ID NO:114)
H	UPATCTCCCTCCAAAAGTGGTGC* (SEQ ID NO:115)	RP-TCCATCTGGAGTACTTTCTGTG* (SEQ ID NO:116)
I	UP-AGTAAATGCTGCAGTTCAGAGG* (SEQ ID NO:117)	RP-CCGTGGCATATCATCCCCC* (SEQ ID NO:118)
J	UP-CCCAGACTGCTTCAAAATTACC* (SEQ ID NO:119)	RP-GAGCCTCATCTGTACTTCTGC* (SEQ ID NO:120)
K	UP-CCCTCCAAATGAGTTAGCTGC* (SEQ ID NO:121)	RP-TTGTGGTATAGGTTTTACTGGTG* (SEQ ID NO:122)
L	UP-ACCCAACAAAAATCAGTTAGATG* (SEQ ID NO:123)	RP-GTGGCTGGTAACTTTAGCCTC* (SEQ ID NO:124)
N	UP-ATGATGTTGACCTTTCCAGGG* (SEQ ID NO:125)	RP-ATTGTGTAACTTTTCATCAGTTGC* (SEQ ID NO:126)
M	UP-AAAGACATACCAGACAGAGGG* (SEQ ID NO:127)	RP-CTTTTTTGGCATTGCGGAGCT* (SEQ ID NO:128)
O	UP-AAGATGACCTGTTGCAGGAATG* (SEQ ID NO:129)	RP-GAATCAGACCAAGCTTGTCTAGAT* (SEQ ID NO:130)
P	UP-CAATAGTAAGTAGTTTACATCAAG* (SEQ ID NO:131)	RP-AAACAGGACTTGTACTGTAGGA* (SEQ ID NO:132)
Q	UP-CAGCCCCTTCAAGCAAACATC* (SEQ ID NO:133)	RP-GAGGACTTATTCCATTTCTACC* (SEQ ID NO:134)
R	UP-CAGTCTCCTGGCCGAAACTC* (SEQ ID NO:135)	RP-GTTGACTGGCGTACTAATACAG* (SEQ ID NO:136)
S	UP-TGGTAATGGAGCCAATAAAAAGG* (SEQ ID NO:137)	RP-TGGGACTTTTCGCCATCCAC* (SEQ ID NO:138)
T	UP-TGTCTCTATCCACACATTCGTC* (SEQ ID NO:139)	RP-ATGTTTTTCATCCTCACTTTTTGC* (SEQ ID NO:140)
U	UP-GGAGAAGAACTGGAAGTTCATC* (SEQ ID NO:141)	RP-TTGAATCTTTAATGTTTGGATTTGC* (SEQ ID NO:142)
V	UP-TCTCCCACAGGTAATACTCCC (SEQ ID NO:143)	RP-GCTACAACTGAATGGGGTACG (SEQ ID NO:144)
W	UP-CAGGACAAAATAATCCTGTCCC (SEQ ID NO:145)	RP-ATTTTCTTACTTTCATTCTTCCTC (SEQ ID NO:146)

All primers are read in the 5' to 3' direction, the first primer in each pair lies 5' of the exon it amplifies: the second primer lies 3' of the exon it amplifies. Primers that lie within the exon are identified by an asterisk. UP represents the 21M13 universal primer sequence[:]. RP represents the M13 reverse primer sequence.

(3) Column 32:

TABLE IV

Seven Different Versions of the 20-Amino Acid Repeat

Consensus:	F * V E * T P * C F S R * S S L S S L S	(SEQ ID NO:147)
1262:	Y C V E D T P I C F S R C S S L S S L S	(SEQ ID NO:148)
1376:	H T V Q E T P L M F S R C T S V S S L D	(SEQ ID NO:149)
1492:	F A T E S T P D G F S C S S S L S A L S	(SEQ ID NO:150)
1643:	Y C V E G T P I N F S T A T S L S D L T	(SEQ ID NO:151)
1848:	T P I E G T P Y C F S R N D S L S S L D	(SEQ ID NO:152)
1953:	F A I E N T P V C P S H N S S L S S L S	(SEQ ID NO:153)
2013:	R H V E D T P V C F S R N S S L S S L S	(SEQ ID NO:154)

Numbers denote the first amino acid of each repeat. The consensus sequence at the top reflects a majority amino acid at a given position.